

FIG. 1

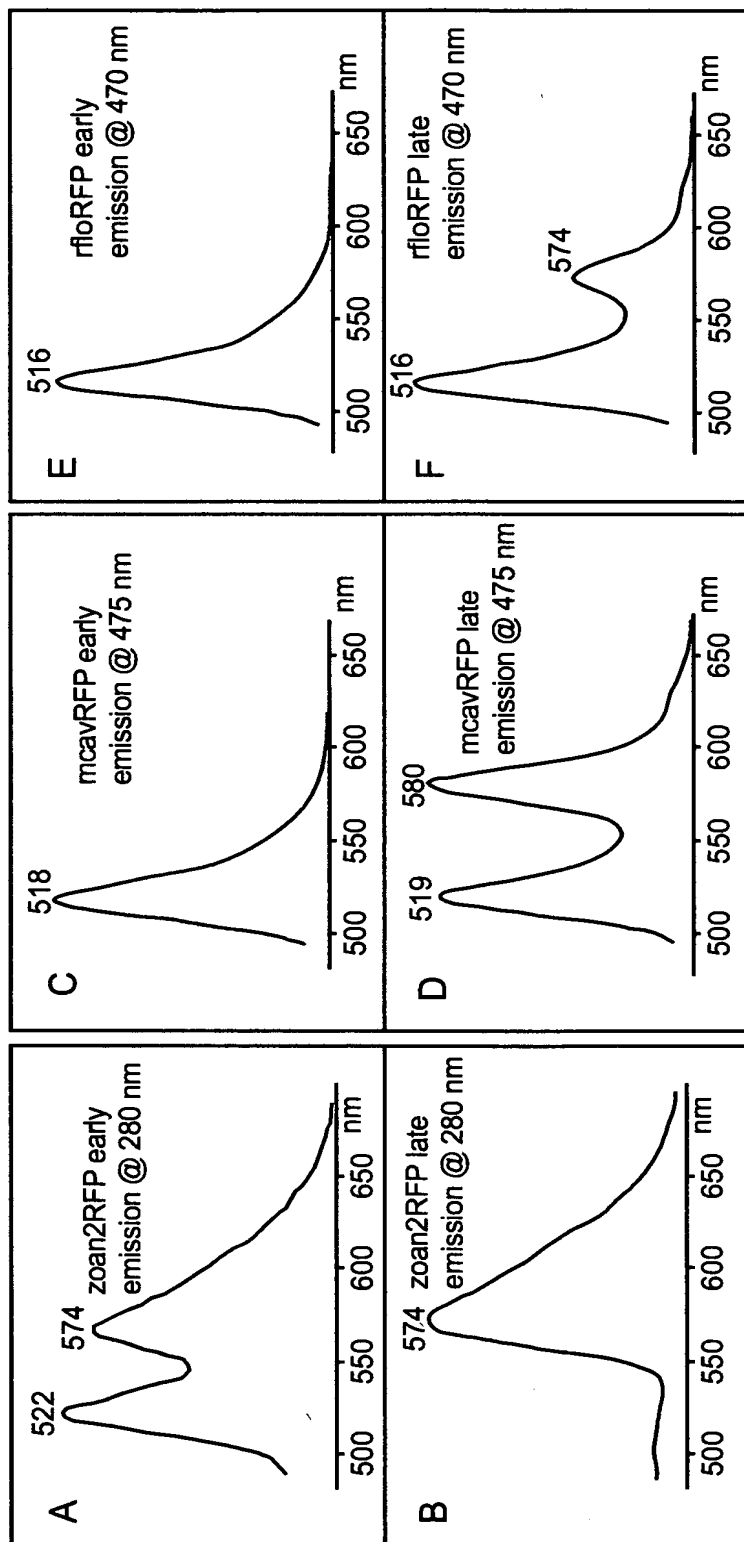


FIG. 2

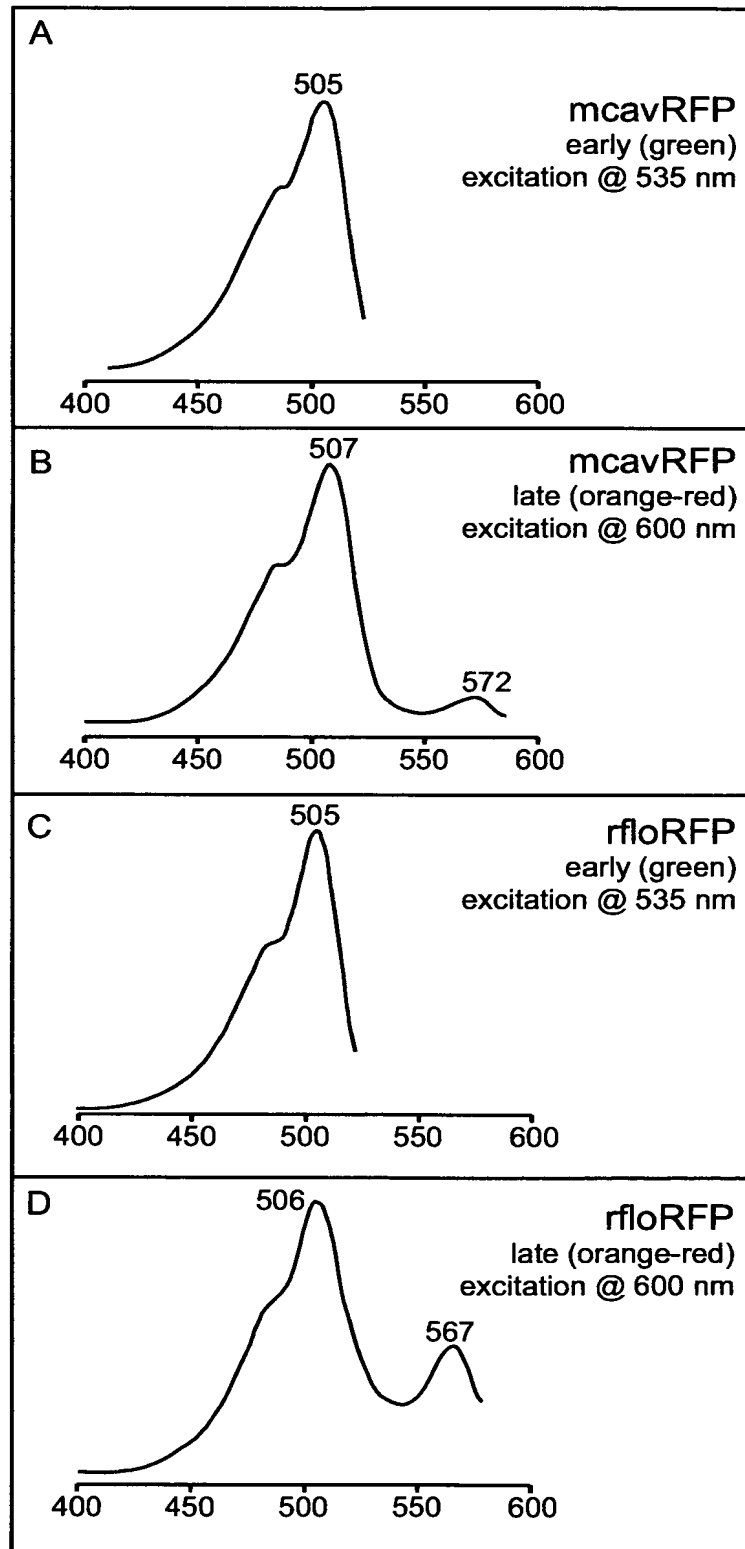


FIG. 3

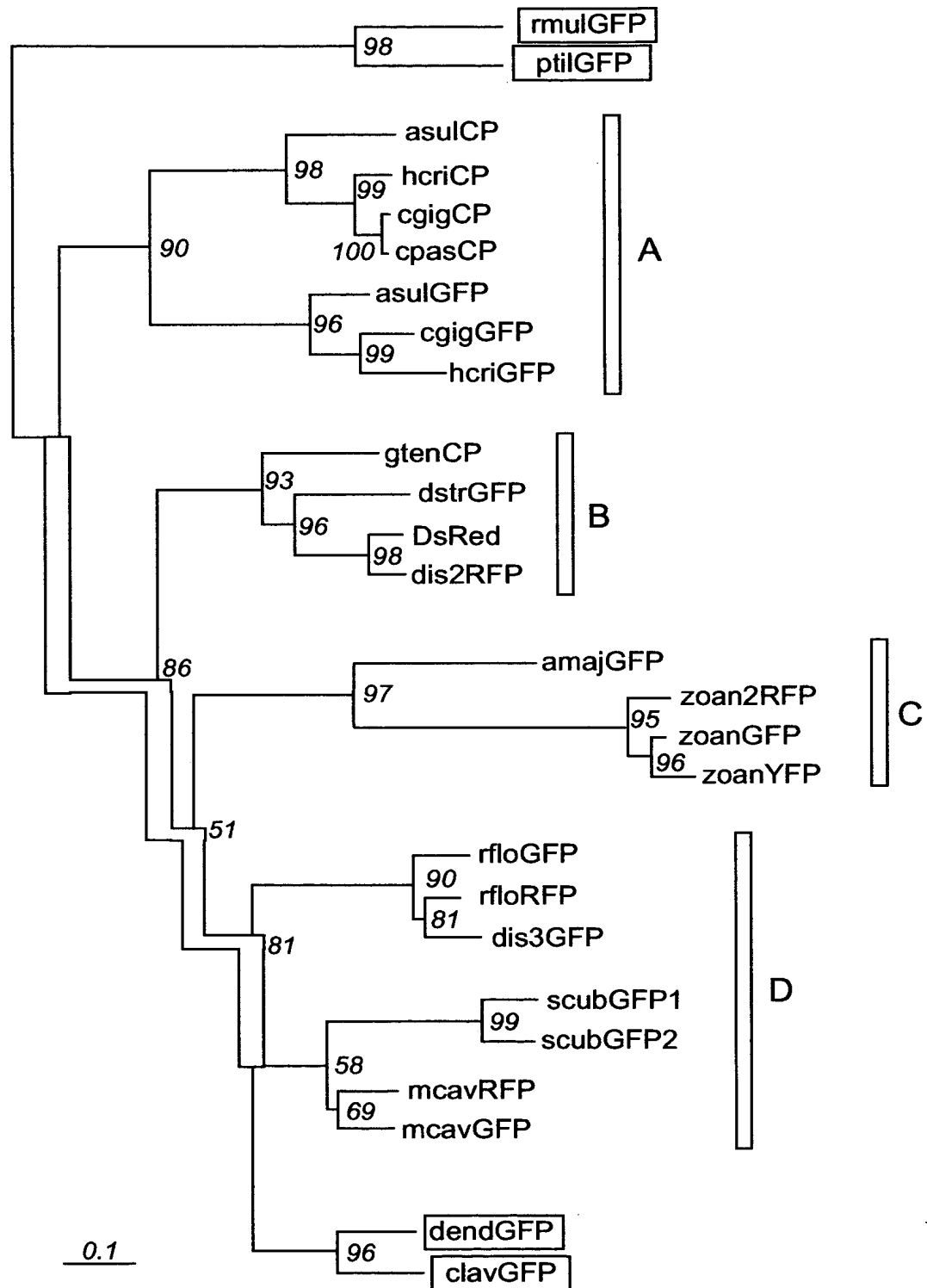


FIG. 4A

Protein ID (original ID)	GenBank accession #	Reference
amajGFP (amFP486) dstrGFP (dsFP483) clavGFP (cFP484)	AF168421 AF168420 AF168424	2 2 2
GFP cgigGFP hcriGFP	M62653 AY037776 AF420592	34 this paper this paper
ptilGFP rmulGFP zoanGFP (zFP506) asulGFP (asFP499) dis3GFP dendGFP mcavGFP rflGFP scubGFP1 scubGFP2	AY015995 AY015996 AF168422 AF322221 AF420593 AF420591 AY037769 AY037772 AY037767 AY037771	35 35 2 4 this paper this paper this paper this paper this paper this paper
zoanYFP (zFP538)	AF168423	2
DsRed (drFP583) dis2RFP (dsFP593) zoan2RFP	AF168419 AF272711 AY059642	2 36 this paper
mcavRFP rflRFP	AY037770 AY037773	this paper this paper
asulCP (asCP)	AF246709	3, 4
hcriCP (hcCP) cgigCP (cgCP) cpasCP (cgCP) gtenCP (gtCP)	AF363776 AF363775 AF383155 AF383156	5 5 5 5

FIG. 4B

Taxonomy <i>Genus species</i> (Class, Sub-class, Order)
<i>Anemonia majano</i> (Anthozoa, Zoantharia, Actiniaria) <i>Discosoma striata</i> (Anthozoa, Zoantharia, Corallimorpharia) <i>Clavularia sp.</i> (Anthozoa, Alcyonaria, Alcyonacea)
<i>Aequorea victoria</i> (Hydrozoa,....., Hydroida) <i>Condylactis gigantea</i> (Anthozoa, Zoantharia, Actiniaria) <i>Heteractis crispa</i> (Anthozoa, Zoantharia, Actiniaria)
<i>Ptilosarcus sp.</i> (Anthozoa, Alcyonaria, Pennatulacea) <i>Renilla muelleri</i> (Anthozoa, Alcyonaria, Pennatulacea) <i>Zoanthus sp.</i> (Anthozoa, Alcyonaria, Zoanthidea) <i>Anemonia sulcata</i> (Anthozoa, Zoantharia, Actiniaria) <i>Discosoma sp.3</i> (Anthozoa, Zoantharia, Corallimorpharia) <i>Dendronephthya sp.</i> (Anthozoa, Alcyonaria, Alcyonacea) <i>Montastraea cavemosa</i> (Anthozoa, Zoantharia, Scleractinia) <i>Ricordea florida</i> (Anthozoa, Zoantharia, Corallimorpharia) <i>Scolymia cubensis</i> (Anthozoa, Zoantharia, Scleractinia) <i>Scolymia cubensis</i> (Anthozoa, Zoantharia, Scleractinia)
<i>Zoanthus sp.</i> (Anthozoa, Zoantharia, Zoanthidea)
<i>Discosoma sp.1</i> (Anthozoa, Zoantharia, Corallimorpharia) <i>Discosoma sp.2</i> (Anthozoa, Zoantharia, Corallimorpharia) <i>Zoanthus sp.2</i> (Anthozoa, Zoantharia, Zoanthidea)
<i>Montastraea cavemosa</i> (Anthozoa, Zoantharia, Scleractinia) <i>Ricordea florida</i> (Anthozoa, Zoantharia, Corallimorpharia)
<i>Anemonia sulcata</i> (Anthozoa, Zoantharia, Actiniaria)
<i>Heteractis crispa</i> (Anthozoa, Zoantharia, Actiniaria) <i>Condylactis gigantea</i> (Anthozoa, Zoantharia, Actiniaria) <i>Condylactis passiflora</i> (Anthozoa, Zoantharia, Actiniaria) <i>Goniopora tenuidens</i> (Anthozoa, Zoantharia, Scleractinia)

FIG. 4C

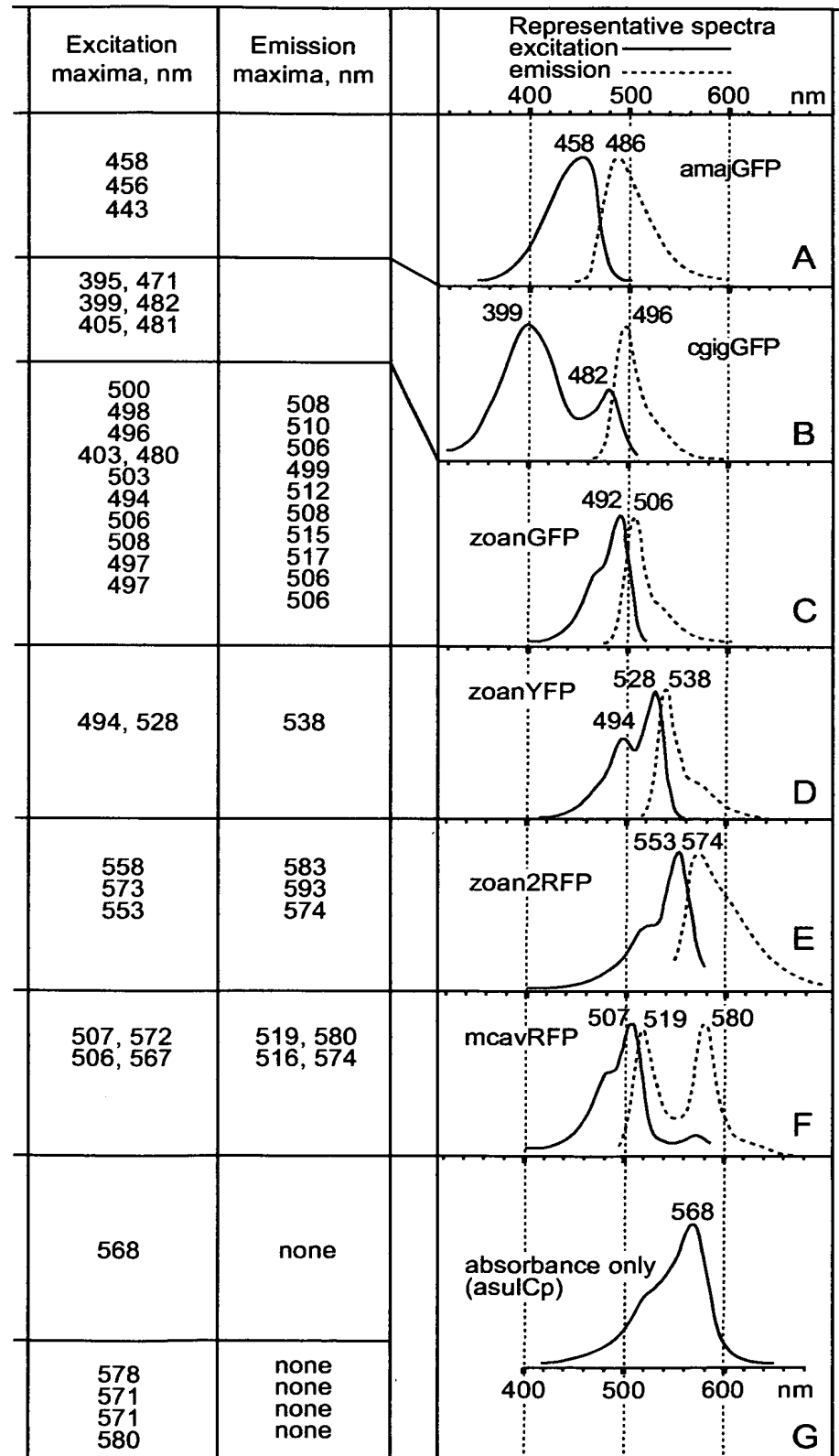


FIG. 4D

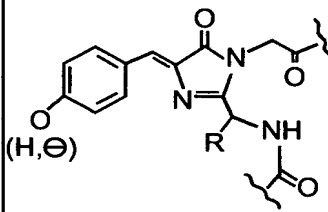
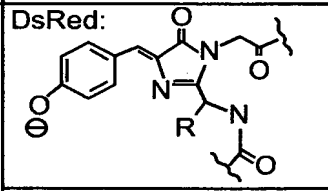
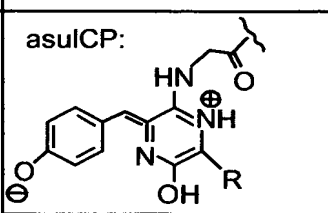
	color	Representative chromophore structure
	GREEN	<p>GFP:</p> 
	YELLOW	?
	ORANGE-RED	<p>DsRed:</p> 
		?
	PURPLE-BLUE	<p>asulCP:</p> 
		?

FIG. 5

Table 2

clade	colors	Zoantharia orders
A	Green, purple-blue	Actiniaria
B	Green, orange-red, purple-blue	Corallimorpharia, Scleractinia
C	Green, yellow, orange-red	Actiniaria, Zoanthidea
D	Green, orange-red	Corallimorpharia, Scleractinia

FIG. 6

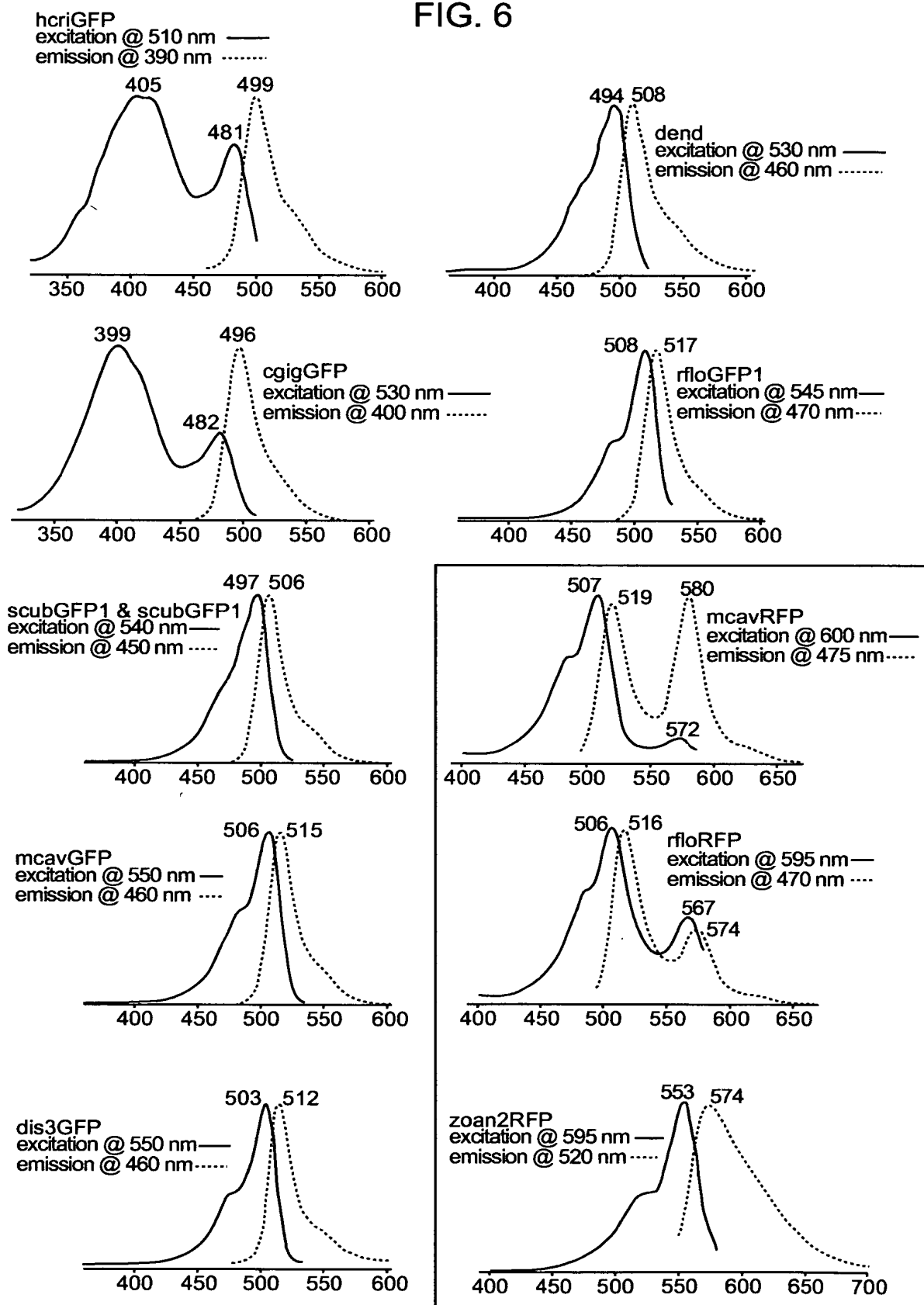


FIG. 7A

	10	20	30	40	50	60									
:	-----MSKGEELFTG-VWPIILVELDGVNGHKFTSVSGEGEDATYKGLILFKICTT-KGLPVP--WPTLVITFSYG						67								
rmulGFP	-----MSKQILKNTCLOE-VMSYKVNLEGTIVNNHVTMEGCGKNILFGNQLVQIRVT--KGAPLPFAFDIVSPAFOYG						71								
ptilGFP	-----MNRNVLKNTGLKE-TMSAKASVEGIVNNHVSMEGFGKENVLFGNQLMQIRVT--KGGPLPFAFDIVSIAFOYG						71								
asulGFP	-----MASFLKK-TMPFKITIEGTVNGHYFKCTGKGEGNPFEGTQEMKIEVI--EGGPLPFAFDILSTSCWYG						65								
hcriCP	-----MAGLLKE-SMRIKMYMEGTVNGHYFKCEGEGDGNPFTGTQSNRIHVT--EGAPLPFAFDILAPCCEYG						65								
cgigCP	-----MAGLLKE-SMRIKIYMEGTVNGHYFKCEGEGDGNPFTGTQSNRIHVT--EGAPLPFAFDILSPCCAYG						65								
cpasCP	-----MAGLLKE-SMRIKIYMEGTVNGHYFKCEGEGDGNPFTGTQSNRIHVT--EGAPLPFAFDILSPCCAYG						65								
asulGFP	-----MYPSTKE-TMRVQLSMEGSWNYHAFKCTGKGEKPYEGTQSLNITIT--EGGPLPFAFDILSHAFQYG						65								
cgigGFP	-----MYPWIKE-TMRSKVYMEGDVNNHAFKCTAVGEGKPYKGSQDLTITVT--EGGPLPFAFDILSHAFQYG						65								
hcriGFP	-----MCSYIKE-TMQSKVYMEGKVDNHNFKCTAEGKGEKPYKGSQSLTITVT--EGGPLPFAFDILSHAFRYG						65								
aasp?FP	-----MSVIAK-QMTYKYVMSGTVNGHYFVEVGDGKG-PYEGETVRLTIVT--KGGPLPFAWDILSPQSOYG						63								
gtenCP	-----MSVIAK-QMTYKYVMSGTVNGHYFVEVGDGKGPYEGEQTIVRLTIVT--KGGPLPFAWDILSPQSOYG						64								
dstrGFP	-----MSCSKSVIKE-EMLIDLHLEGTFNHGYFEIKGKGQPNEGTIVTLEVT--KGGPLPFGWHILCPQFOYG						68								
DisRed	-----MRSSKNVIKE-FWRFKVRMEGTVNGHFEIEGEGEGRPYEGHNTVKLKVT--KGGPLPFAWDILSPQOYQY						68								
dis2RFP	-----MSCSKNVIKE-FWRFKVRMEGTVNGHFEIEKGEGRPYEGHCSVKLMVT--KGGPLPFAFDILSPQOYQY						68								
amajGFP	-----MALSNKFIGD-DKMTYHMDGCVNGHYFTVKEGNGKPYEGTQTSFKVTMANGGPLAFSFDILSTVFKYG						70								
zoanGFP	-----MAQSKHGLTK-EMTMKYRMEGCVDGHKFVITGEGIGYPFKGQAINLCVW--EGGPLPFAEDILSAAFNYG						68								
zoanYFP	-----MAHSHKHGLKE-EMTMKYRMEGCVNGHGFVITGEGIGYPFKGKQTNLCVI--EGGPLPFSEDILSAGFKYG						68								
zoan2RFP	-----MAHSHKHGLTD-DMTMHRMEGCVDGHKFVIEGNGNGNPFKQFINLCVI--EGGPLPFSEDILSAAFDYG						68								
rflorFP	-----MSALKE-EMKIKLTLGVVNGHPFKIIGDGKGPYEGSQELTLAV--EGGPLPFSDILTTIVHYG						64								
rflorGFP	-----MSALKE-EMKIKLRWGVVNGSQFDIDGEGKGPYEGSQKLTLEW--EGGPLLFSYDILTTIFQYG						64								
dis3GFP	-----MSALKE-YMKINLTMEGVNGLPFKIRGDGKGPYQGSQELTLTV--KGGPLPFSYDILTTMFQYG						64								
scubGFP1	-----MQRAGWKVKE-HMKIKLRMGTVNGKHPAVNGTGDGYPYQKGQILKLIVE--GSEPLPFAFDILSAAFOYG						68								
scubGFP2	-----MQSAGKKNVVD-FMRIITLRMDGAVNGKPPAVNGTGNPNYGGIQSILKLTVD--GNKPLPFAFDILSAAFOYG						70								
mcavRFP	-----MSVKS-YMKIKLRMEGSWNGHNFVITVEGEGKPYEGTQSMDLTVK--EGAPLPFAVDIMTIVFHYG						64								
mcavGFP	-----MTSVAQEGVVKP-DMKMKLRMEGAVNGHGFVEGDKGKPFDTGTQTNDLTVI--EGAPLPFAVDILTTVFDYG						71								
dendGFP	-----MNLIKE-DMRVKVMNEGVNNGHAFVIEGEGKRPYEGTQTLNLTIVK--EGAPLPFSYDILTTALHYG						64								
clavGFP	-----MKCKFVFCLSFLVLAITNANIFLRNEADLEEKTLRIPKALTITMGVVKPDMKIKLRMEGVNNGHAFVIEGEGKPYDGTHTLINLEVK--EGAPLPFSYDILSNAFOYG						106								
	6	6	G	vlgh	F	g	G	G	p	G	q	g	P6pf	di6	YG

FIG. 7B

	70	80	90	100	110	120	130	140	150	160	
GFP	: VQCFSRYPDHMKQHDFFKSAM---	PEGYVQERTIFYKDDGNKSAEAVKFEGD---	TLVNRTELKGIIDFKEDGNILGHKMEYNYNSHNVIYIMADKQKNGIKVNFKIRH	: 169							
mtulGFP	: NRFTTKYPNDIS--DYFIQSF--	PAGFMVYERTLRYEDGGLVEIRSDINLIED---	KFYRVVEYKGSNFFDDGPVM-QKTTILGIEPSFEAMVM--	NNGLVGEVILVY : 168							
ptilGFP	: NRFTTKYPDDIA--DYFQSF--	PAGFFYERINLRFEDGAIVDIRSDISLEDD---	KFYKVEYKGSNFFDDGPVM-QKAILGWEPSFEVVM--	NSGVLVGEVDLVY : 168							
asulGFP	: SKTFIKYVSGIP--DYFQSF--	PEGFTWERTITYEDGGFLTAHQDTSLEGD---	CLVYKVKILGNFPADGPVM-QNKAGRWEPEATEIVYE--	VDGVLRGQSIMAL : 162							
hcriCP	: SRTFVHHTAEIP--DFFQSF--	PEGFTWERTITYEDGGILTAHQDTSLEGN---	CLLYKVKVLGTNFPADGPVM-KNKSQGWEPCTEIVVP--	ENGVLGRNVMAL : 162							
cgigCP	: SKTFIKHTSGIP--DYFQSF--	PEGFTWERTITYEDGGVLTAAHQDTSLEGN---	CLLYKVKVLGTNFPADGPVM-KKLSQGWEPCTEIVYQ--	DNGVLGRNVMAL : 162							
cpasCP	: SKTFIKHTSGIP--DYFQSF--	PEGFTWERTITYEDGGVLTAAHQDTSLEGN---	CLLYKVKVLGTNFPADGPVM-KNLSQGWEPCTEIVYQ--	DNGVLGRNVMAL : 162							
asulGFP	: IKVFAKYPKEIP--DFFQSL--	PGGFSWERVSTYEDGGVLSATQETSLEQD---	CLICVKVLGTNFPADGPVM-QKKTGWEPSSETVIP--	RDGGLLRDTPAL : 162							
cgigGFP	: NKVFTDYPDDIP--DFFQSL--	SDGFTWRRVSNYDDGGVLTAAHQDTSLEQD---	CLICNIVKHGTNFPADGPVM-QKKTGWEPSSETVIP--	QDGGIIVAAASPAL : 162							
hcriGFP	: NKVFAKYPKDHIP--DFFQSL--	PEGFTWRRVSNYDDGGVLTAAHQDTSLEQD---	CLICNIVKHGTNFPADGPVM-QKKTGWEPSSETVIP--	QDGGIIVAAASPAL : 162							
asp?FP	: SIPFTKYPEDIP--DYVKQSF--	PEGYTWERIMNIFEDGAVCTVSNDSIQGN---	CFIYHVKFSGLNFPADGPVM-QKKTGWEPTETERLFA--	RDGMLIGNNFMAL : 159							
gtenCP	: SIPFTKYPEDIP--DYVKQSF--	PEGYTWERIMNIFEDGAVCTVSNDSIQGN---	CFIYHVKFSGLNFPADGPVM-QKKTGWEPTETERLFA--	RDGMLIGNNFMAL : 161							
dstrGFP	: NKAFVHHPDNIH--DYLKLSF--	PEGYTWERSMHIFEDGGLCCIITNSIDLITGN---	CFYVDIKFTGLNFPADGPV--QKKTGWEPSSTERLYP--	RDGVLIGEDIHHAH : 165							
DsRed	: SKVYVVKHPADIP--DYKKLSF--	PEGFKWERVMNIFEDGGVWTVTQDSSLQDG---	CFIYKVKFIGNFPADGPVM-QKKTGWEPTETERLYP--	RDGVLIGEDIHHAH : 165							
dis2RFP	: SKVYVVKHPADIP--DYKKLSF--	PEGFKWERVMNIFEDGGVWTVTQDSSLQDG---	CFIYKVKFIGNFPADGPVM-QKKTGWEPTETERLYP--	RDGVLIGEDIHHAH : 165							
amajGFP	: NRCTAYPTSMIP--DYFKQAF--	PDGMSYERTITYEDGGVATASWEISLQGN---	CFEYHKSITHGVNFPADGPVM-QKKTGWDPSFEKMTV--	CDGLILKGDVTAFL : 167							
zoanGFP	: NRVTIEYQDIV--DYFNKSC--	PAGYTWDRSFLFEDGAVCI CNADITVSVE--	ENCMYHESKFYGVNFPADGPVM-KKMTDNWEPSTEIMV--	QGVILKGEVSMYL : 169							
zoanYFP	: DRIFTEYQDIV--DYFNKSC--	PAGYTWGRSFLFEDGAVCI CNVDITVSVK--	ENCIYHKSIFGNMFPADGPVM-KKMTTNWEASCEKIMPVKQILKGDVSMYL	: 169							
zoan2RFP	: NRLETEYPEGIV--DYFNKSC--	PAGYTWGRSFLFEDGAVCI CSADITVNR--	ENCIYHESITFYGVNFPADGPVM-KKMTTNWEPSTEIMV--	INSQKTLKGDVSMYL : 169							
rflorFP	: NRFAVNYPKDIP--DIFKQCSGPAGYSQRTMSFEDGGVCTATSHIRVDGD---	TFNYD IHFMGADFPDGPVM-QKRTVKEPSTEIMFQ--	CDGLLRGDAVMSL : 164								
rflorGFP	: NRFAVNYPKDIP--DIFKQCSGPAGYSQRTMSFEDGGVCTATSHIRVDGD---	TFNYD IHFMGADFPDGPVM-QKRTVKEPSTEIMFQ--	CDGLLRGDAVMSL : 164								
dis3GFP	: NRFAVNYPKDIP--DIFKQCSGPAGYSQRTMSFEDGGVCTATSHIRVDGD---	TFNYD IHFMGADFPDGPVM-QKRTVKEPSTEIMFQ--	CDGLLRGDAVMSL : 164								
scubGFP1	: NRFAVNYPKDIP--DIFKQCSGPAGYSQRTMSFEDGGVCTATSHIRVDGD---	TFNYD IHFMGADFPDGPVM-QKRTVKEPSTEIMFQ--	CDGLLRGDAVMSL : 164								
scubGFP2	: NRFAVNYPKDIP--DIFKQCSGPAGYSQRTMSFEDGGVCTATSHIRVDGD---	TFNYD IHFMGADFPDGPVM-QKRTVKEPSTEIMFQ--	CDGLLRGDAVMSL : 164								
mcavRFP	: NRFAVNYPKDIP--DIFKQCSGPAGYSQRTMSFEDGGVCTATSHIRVDGD---	TFNYD IHFMGADFPDGPVM-QKRTVKEPSTEIMFQ--	CDGLLRGDAVMSL : 164								
mcavGFP	: NRFAVNYPKDIP--DIFKQCSGPAGYSQRTMSFEDGGVCTATSHIRVDGD---	TFNYD IHFMGADFPDGPVM-QKRTVKEPSTEIMFQ--	CDGLLRGDAVMSL : 164								
dendGFP	: NRFAVNYPKDIP--DIFKQCSGPAGYSQRTMSFEDGGVCTATSHIRVDGD---	TFNYD IHFMGADFPDGPVM-QKRTVKEPSTEIMFQ--	CDGLLRGDAVMSL : 164								
clavGFP	: NRFAVNYPKDIP--DIFKQCSGPAGYSQRTMSFEDGGVCTATSHIRVDGD---	TFNYD IHFMGADFPDGPVM-QKRTVKEPSTEIMFQ--	CDGLLRGDAVMSL : 164								

yp D fk p g R 5edg G Fp 1Gp66 ep e 6 g 6 g 1

FIG. 7C

	170	180	190	200	210	220	230	
GFP	: NLEDG-SVQLADHYQONTPIGDG-PVLLPDNHYLSTQSA	LKSDPNEKRDMILLEFVTAAGITHGMDLYK-----	: 238					
rmulGFP	: KLSNG-KYYSCHMKTLMKSGV--VKEFPSYHFIOHRLEKTYVEDGG--FVEQHETAIAQMTSIGKPLGSLHEWV-----	: 238						
ptilGFP	: KLESQ-NYYSCHMKTfYRSKGG--VKEFPEYHFfIHRLEKTYVEEGS--FVEQHETAIAQLTITIGKPLGSLHEWV-----	: 238						
asulGFP	: KCPGG-RHLTCHLHTTYRSKKPASALKMPGFHFDHRIEIMEEVEKKG-CYQYEAAGVGRYCDAAPSKLGHN-----	: 232						
hcriCP	: KVGDR--RLICHLYTSYRSKKAVRALTMPGFHFDIRLQMPRKKKDE--YFELYEASVARYSDLPKAN-----	: 227						
cgigCP	: KVSGR-PPLICHLHSTYRSKK-ACALTMPGFHFDLRIOMPKKKDE--YFELYEASVARYSDVPEKAT-----	: 227						
cpasCP	: KVSGR-PPLICHLHSTYRSKK-ACALTMPGFHFDLRIOMPKKKDE--YFELYEASVARYSDLPKAN-----	: 227						
asulGFP	: MLADG-GHLSCFMETTYKSKK----EVKLPELHFFHLRMEKLNISDDWK-TVEQHEVAVASYSQVPSKLGHN-----	: 228						
cgigGFP	: RLADK-GHLICHMETTYKPNK----EVKLPELHFFHLRMEKLSVSDDGK-TIKQHEVAVASYSKVPKIGRQW-----	: 229						
hcriGFP	: KLGNKGHLICVNETTYKSKK----KVNLPKPHFHLRMEKOSVSDDEK-TIEQHENVRASYFNDGSK-----	: 225						
aasp?FP	: KLEGG-GHYLCEPKSTYKAKK----PVRMPGYHYVDRKLDVTNHNKDYT-SVEQCEISIAARKPVVA-----	: 219						
gtenCP	: KLEGG-GHYLCEPKSTYKAKK----PVRMPGYHYVDRKLDVTNHNIDYT-SVEQCEISIAARKPVVA-----	: 221						
dstrGFP	: TVEGG-GHYACDIKTIVYRAKKA--ALKMPGYHYVDTKLVIWNNDKEFM-KVEEHEIAVARHHPFYPEKKDK-----	: 232						
DsRed	: KLDG-GHYLVEPKSIYMAKK----PVQLPGYVYVDSKLDITSHNEDYT-IVEQYERTEGRHHLFL-----	: 225						
dis2RFP	: RLEGG-GHYLVEPKSIYMWKK--PSVQLPGYVYVDSKLDMTSHNEDYT-VEQVEKTQGRHHPFIKPL-----	: 229						
amajGFP	: MLQGG-GNYRCQFHTSYTKTK----PVTMPPNHVVEHRIARTDLDKGGN-SVQLTEHAVAHITSVF-PF-----	: 229						
zoanGFP	: LLDKG-GRLCQFDTVYKAKSV--PRLMPDWHFIQHKLTREDRSDAKNQKWLTHEAIAAGSALP-----	: 231						
zoanYFP	: LLDKG-GRYRCQFDTVYKAKSV--PSKMPDWHFIQHKLLREDRSDAKNQKWLTHEAIAFPSALA-----	: 231						
zoan2RFP	: LLDKG-GRYRCQFDTIYKAKTE--PKMPDWHFIQHKLNREDRSDAKNQKWLTHEAIAASRSALP-----	: 231						
rfloRFP	: LLDKG-GHYRCDFKTIYKPKK----NVKMPGYHFDHCIEITSQDDYN-VVELYEGAVAHYSPLQKPCQAKA-----	: 231						
rfloGFP	: LLDKG-GHYRCDFKTIYTPKR----KVNMPGYHFDHCIEIOKHKDYN-MAVLSEDAVAHNSPLEKKSQAKA-----	: 231						
dis3GFP	: LLDKG-GHYRCDFETIYKPNK----VKMPDYHFDHYIEITSQNYN-VVELTEVAEARYSLSLEKIGSKA-----	: 231						
scubGFP1	: LLDQK-SHYRCDLKTYYKAKNNVP--HPPGYHYVDHCIEILEERKDH--VKLREHAKARSSLSPTSAKERKA-----	: 234						
scubGFP2	: LLDKQ-SHYRCDFKTIYKAKNPVPTALPDYHYVDHCIEITEENRDY--VNLQYAKARSGHLHLPKLQK-----	: 235						
mcavRFP	: LLEGG-GHYRCDFRTYRAKKK--GVKLDPYHFDHDSIEILRHDKYET-EVKLYEHAEAHSGLPRGORKA-----	: 227						
mcavGFP	: LLEGG-GHYRCDFKTIYKAKK----VWRLPDYHFDHRIEIVSHDKDYN-KVKLHEHAEARHGLSRKAK-----	: 234						
dendGFP	: LLEGG-GHYLCDFKTIYKAKK----VWQLPDYHFDHRIEILSNDSDYN-KVKLYEHGVARYSPLPKSGLVEVQKAIMTA	: 236						
clavGFP	: LLEGG-GHYRCDFKSIYKAKK--VVKLPDYHFDHRIEILNHDKDYN-KVILYENAVARYSLL--PSQA-----	: 266						

c y k p h E a

FIG. 8

Green fluorescent protein from *Heteractis crispa* hcriGFP

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      10      20      30      40      50      60
ATTTTGGACAGGTGTTCAACCAAGCAAATTTAAGAAGTCATCATCTTTATCTCAGTCAGG

      70      80      90     100     110     120
AAAATGTGTTCTTACATCAAAGAAACCATGCAAAGTAAGGTTTACATGGAAGGAAAAGTT
  M  C  S  Y  I  K  E  T  M  Q  S  K  V  Y  M  E  G  K  V

     130     140     150     160     170     180
AACGACCACAACTTCAAGTGCACTGCAGAAGGAAAAGGAGAACCATACAAAGGCTCACAA
  N  D  H  N  F  K  C  T  A  E  G  K  G  E  P  Y  K  G  S  Q

     190     200     210     220     230     240
AGCCTGACGATCACCGTAACTGAAGGAGGTCCTCTGCCATTTCGCTTCGACATTCTTTCA
  S  L  T  I  T  V  T  E  G  G  P  L  P  F  A  F  D  I  L  S

     250     260     270     280     290     300
CACGCCTTTTCGATATGGCAATAAGGTGTTTCGCCAAGTACCCCAAAGATCATCCTGATTTT
  H  A  F  R  Y  G  N  K  V  F  A  K  Y  P  K  D  H  P  D  F

     310     320     330     340     350     360
TTTAAGCAGTCTCTTCCTGAAGGTTTTACTTGGGAAAGAGTAAGCAACTATGAGGACGGA
  F  K  Q  S  L  P  E  G  F  T  W  E  R  V  S  N  Y  E  D  G

     370     380     390     400     410     420
GGAGTCCTTACCGTTAAACAAGAACTAGTCTGGAGGGAGATTGCATTATTTGCAAAATT
  G  V  L  T  V  K  Q  E  T  S  L  E  G  D  C  I  I  C  K  I

     430     440     450     460     470     480
AAAGCACATGGCACTAACTTCCCCGCAGATGGTCCGGTGATGCAAAAACGGACCAATGGA
  K  A  H  G  T  N  F  P  A  D  G  P  V  M  Q  K  R  T  N  G

     490     500     510     520     530     540
TGGGAGCCATCAACTGAAACGGTTATTCACGGGGTGGAGGAATTCTGATGCGCGATGTG
  W  E  P  S  T  E  T  V  I  P  R  G  G  G  I  L  M  R  D  V

     550     560     570     580     590     600
CCCGCACTGAAGCTGCTTGGTAACAAAGGACATCTTCTCTGCGTCATGGAAACAACTTAC
  P  A  L  K  L  L  G  N  K  G  H  L  L  C  V  M  E  T  T  Y

     610     620     630     640     650     660
AAGTCAAAAAAAAAAAGGTGAACCTGCCAAACCGCACTTTCATCATTTGAGAATGGAGAAG
  K  S  K  K  K  G  E  P  A  K  P  H  F  H  H  L  R  M  E  K

     670     680     690     700     710     720
GATAGTGTTAGTGACGATGAGAAGACCATTGAGCAGCAGAGAATGTGAGGGCAAGCTAC
  D  S  V  S  D  D  E  K  T  I  E  Q  H  E  N  V  R  A  S  Y

     730     740     750     760     770     780
TTCAATGATAGTGGAAAATGATCATTTTCCTTATTGATTTCAATGTTAGGGCATTCAGTTT
  F  N  D  S  G  K  *

     790     800     810     820     830     840
CCAAATTTTCTTAGACACAGTCTTTTCCTTTAGCTTCGTAGCCTACTTACCCATGTTTTG

     850     860
TTGAAGTCAATAAATAGCTAAGCACTAC (SEQ ID NOS: 01 & 02)
```

FIG. 9

Green fluorescent protein from *Dendronephthya* sp. dendGFP

```

      10      20      30      40      50      60
5' CATATCGAGAAAGTTGTGAAACCAAATTCTTACTCTACTTTTACTACCATGAATCTGATT
                                     M N L I

      70      80      90     100     110     120
AAAGAAGATATGAGGGTTAAGGTGCATATGGAAGGGAATGTAAACGGGCATGCTTTTGTG
K E D M R V K V H M E G N V N G H A F V

     130     140     150     160     170     180
ATTGAAGGGGAAGGAAAAGGAAGGCCCTACGAAGGGACACAGACCTTGAACCTGACAGTG
I E G E G K G R P Y E G T Q T L N L T V

     190     200     210     220     230     240
AAAGAAGGCGCGCCTCTCCCATTTTCTTACGACATCTTGACAACAGCATTGCACTACGGA
K E G A P L P F S Y D I L T T A L H Y G

     250     260     270     280     290     300
AACAGAGTATTTCACTGAATACCCAGCAGATATCACGGATTATTTCAAGCAATCATTTCTT
N R V F T E Y P A D I T D Y F K Q S F P

     310     320     330     340     350     360
GAAGGATATTCCTGGGAAAGAACCATGACTTATGAAGACAAGGGCATTGTACCATCAGA
E G Y S W E R T M T Y E D K G I C T I R

     370     380     390     400     410     420
AGCGACATAAGCTTGGAAGGTGACTGCTTTTTTCCAAAACATTTCGTTTTTAATGGGATGAAC
S D I S L E G D C F F Q N I R F N G M N

     430     440     450     460     470     480
TTTCCCCCAAATGGTCCAGTTATGCAGAAGAAAACTTTGAAGTGGAACCATCCACAGAG
F P P N G P V M Q K K T L K W E P S T E

     490     500     510     520     530     540
AAGCTGCACGTGCGTGATGGGTTGCTTGTCGGTAATATTAACATGGCTCTGCTGCTTGAA
K L H V R D G L L V G N I N M A L L L E

     550     560     570     580     590     600
GGAGGTGGACATTACCTGTGTGACTTCAAACTACTTACAAAGCGAAGAAGGTTGTTTCAG
G G G H Y L C D F K T T Y K A K K V V Q

     610     620     630     640     650     660
TTGCCAGATTATCATTTTGTGGACCATCGCATTGAGATCTTGAGTAATGACAGCGATTAC
L P D Y H F V D H R I E I L S N D S D Y

     670     680     690     700     710     720
AACAAAGTGAAGCTGTACGAGCATGGGGTTGCTCGCTATTCTCCGTTGCCCAAGTCAGGC
N K V K L Y E H G V A R Y S P L P K S G

     730     740     750     760     770     780
CTGGTAGAGGTTCAAGGGAAAGCCATAATGACTGCATAGATAAACATGTAGTGAAGACCA
L V E V Q G K A I M T A *

     790     800     810     820     830     840
CATACTCGGGATTAGAGTTTAGGGATTGGTAGTTGTGGTAGATTCTAGCCTACAAATTTT

```

TTGGG 3' (SEQ ID NO:03 & 04)

FIG. 10

Red fluorescent protein from *Zoanthus sp.* zoanRFP

```

      10      20      30      40      50      60
GAGTTGAGTTCTCGACTTCAGTTGTATCACTTTTGACGTATCAAGTGATCTATTCTCAAC

      70      80      90     100     110     120
ATGGCCCATTCAAAGCACGGACTAACAGATGACATGACAATGCATTTCCGTATGGAAGGG
M A H S K H G L T D D M T M H F R M E G

     130     140     150     160     170     180
TGCCTCGATGGACATAAGTTTGTAATCGAGGGCAACGGCAATGGAAATCCTTTCAAAGGG
C V D G H K F V I E G N G N G N P F K G

     190     200     210     220     230     240
AAACAGTTTATTAATCTGTGTGTGATTGAAGGAGGACCACTGCCATTCTCCGAAGACATA
K Q F I N L C V I E G G P L P F S E D I

     250     260     270     280     290     300
TTGTCTGCTGCGTTTGACTACGGAAACAGGCTCTTCACTGAATATCCTGAAGGCATAGTT
L S A A F D Y G N R L F T E Y P E G I V

     310     320     330     340     350     360
GACTATTTCAAGAACTCGTGTCTGCTGGATATACGTGGCACAGGTCTTTTCGCTTTGAA
D Y F K N S C P A G Y T W H R S F R F E

     370     380     390     400     410     420
GATGGAGCAGTTTGCATATGCAGTGCAGATATAACAGTAAATGTTAGGGAAAACCTGCATT
D G A V C I C S A D I T V N V R E N C I

     430     440     450     460     470     480
TATCATGAGTCCACGTTTTATGGAGTGAACTTTCCTGCTGATGGACCTGTGATGAAAAAG
Y H E S T F Y G V N F P A D G P V M K K

     490     500     510     520     530     540
ATGACAACATAATTGGGAACCGTCCTGCGAGAAAATCATACCAATAAATAGTCAGAAGATA
M T T N W E P S C E K I I P I N S Q K I

     550     560     570     580     590     600
TTAAAAGGGGATGTCTCCATGTACCTCCTTCTGAAGGATGGTGGGCGTTACCGCTGCCAG
L K G D V S M Y L L L K D G G R Y R C Q

     610     620     630     640     650     660
TTTGACACAATTTACAAAGCAAAGACTGAGCCAAAAGAAATGCCGGACTGGCACTTCATC
F D T I Y K A K T E P K E M P D W H F I

     670     680     690     700     710     720
CAGCATAAGCTCAACCGTGAAGACCGCAGCGATGCTAAGAATCAGAAATGGCAACTGATA
Q H K L N R E D R S D A K N Q K W Q L I

     730     740     750     760     770     780
GAACATGCTATTGCATCCCGATCTGCTTTACCCTGATAACAAAGGAGTTGCTATTGCATG
E H A I A S R S A L P *

     790     800     810     820     830     840
TGCATGCCTATTACGCTGATAAAAATGTAGTTTAAACATGCAATTGTATGTGCATGCACA

     850
TTACCCTGATA
      (SEQ ID NOS:05 & 06)
```

FIG. 11

Green fluorescent protein from *Scolymia cubensis* scubGFP1 (AY037767)

```

      10      20      30      40      50      60
5' TGTGACATTCAGTCATATAGGAGCCTCTATCGGAGCTGAGGTCCCATTACCGTTGTGAT
      70      80      90     100     110     120
   TTGGACGGGAGCAGATCGAGAACAACMAGGGCTGTACGAGTCTGATAATTTACTTTACAT
      130     140     150     160     170     180
   CTACCAACATGCAGCGTCTGGGATGAAGGTTAAGGAACATATGAAGATCAAACCTGCGTA
      M   Q   R   A   G   M   K   V   K   E   H   M   K   I   K   L   R   M

      190     200     210     220     230     240
   TGGGAGGTACTGTAAACGGAAGCATTTCGCGGTTAATGGGACAGGAGACGGCTACCCTT
      G   G   T   V   N   G   K   H   F   A   V   N   G   T   G   D   G   Y   P   Y

      250     260     270     280     290     300
   ATCAGGGAAAACAGATTTTGAAACTTATCGTCTGAAGGCAGCGAACCTCTGCCTTTTCGCTT
      Q   G   K   Q   I   L   K   L   I   V   E   G   S   E   P   L   P   F   A   F

      310     320     330     340     350     360
   TTGATATCTTGTCTCAGCAGCATTCCAGTATGGCAACAGGGCATTACCGAATACCCAACAG
      D   I   L   S   A   A   F   Q   Y   G   N   R   A   F   T   E   Y   P   T   E

      370     380     390     400     410     420
   AGATAGCAGACTATTTCAAGCAGTCGTTTGTGCGAGGGGTTCTCCTGGGAACGAA
      I   A   D   Y   F   K   Q   S   F   E   F   G   E   G   F   S   W   E   R   S

      430     440     450     460     470     480
   GTTTCACTTTTCGAAGATGGGGCCATTTCGCTCGCCACCAACGATATAACGATGGTTGGTG
      F   T   F   E   D   G   A   I   C   V   A   T   N   D   I   T   M   V   G   G

      490     500     510     520     530     540
   GTGAGTTTCAGTATGATATTCGATTTGATGGTCTGAACTTCCCTGAAGATGGTCCAGTGA
      E   F   Q   Y   D   I   R   F   D   G   L   N   F   P   E   D   G   P   V   M

      550     560     570     580     590     600
   TGCAAAAGAAAACCGTAAAATGGGAGCCATCCACTGAGATAATGTATATGCAAAATGGAG
      Q   K   K   T   V   K   W   E   P   S   T   E   I   M   Y   M   Q   N   G   V

      610     620     630     640     650     660
   TGCTGAAGGGTGAGGTTAACATGGCTCTGTTGCTTCAAGACAAAAGCCATTACCGTTGCG
      L   K   G   E   V   N   M   A   L   L   L   Q   D   K   S   H   Y   R   C   D

      670     680     690     700     710     720
   ACCTCAAACCTACTTACAAAGCTAAGAATAATGTGCCGCATCCTCCAGGCTACCACTATG
      L   K   T   T   Y   K   A   K   N   N   V   P   H   P   P   G   Y   H   Y   V

      730     740     750     760     770     780
   TGGATCACTGCATTGAAATACTCGAAGAACGTAAGGATCACGTTAAGCTGCGGGAGCATG
      D   H   C   I   E   I   L   E   E   R   K   D   H   V   K   L   R   E   H   A

      790     800     810     820     830     840
   CTAAGCTCGTTCTAGCCTGTCACCTACCAGTGCAAAAGAACGAAAGGCTTAGGTGATAG
      K   A   R   S   S   L   S   P   T   S   A   K   E   R   K   A   *

      850     860     870     880     890     900
   TCAAAAAGACAACAAGACGAAAATGAAAGGTGTTTCATTGTTAGAAATTTGATATTTTCGAT
      910     920     930     940     950     960
   TCAATGATTTCGTTAAGGGATTGCTAGAGGCTAGCTAACAGGTTAACATCATAAGGATAG
      970     980     990     1000    1010    1020
   AGATTTCGTTGCGGAGTTAGAACCTTWTATTTTTCCGAATTCCAMCTAGAGTCGTTGAGA
      1030    1040    1050    1060    1070    1080
   AATTTATTAGAGACTAGCTTTAGAGTTACTTTTGTGGAAGAAAAGGTTTCCATTTTTTGC
      1090    1100    1110    1120    1130    1140
   GTTATTACAGCATTTAAAGCATAGGAATAGAGATTTCGGTTATGGAAAATAACAGTAGGAA
      1150    1160    1170
   AATACGTTGTGAAAATAAACTTGTTCGAAAAAAA 3'

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(SEQ ID NOS:07&08)

FIG. 12

Green fluorescent protein from *Scolymia cubensis* scubGFP2 (AY037771)

```

      10      20      30      40      50      60
5' CCTGGTGATTTGGACGAGAGCAGATCGAGAATAGCAAGGTTTTACCAGCGTGATAATTTA
      70      80      90     100     110     120
   CTTTACATCTAACAACATGCAATCTGCTGGGAAGAAGAATGTCGTTAAGGACTTCATGAA
      M  Q  S  A  G  K  K  N  V  V  K  D  F  M  K

      130     140     150     160     170     180
   GATCACACTGCGTATGGACGGTGCTGTAAACGGGAAGCCCTTCGCGGTTAATGGAACAGG
      I  T  L  R  M  D  G  A  V  N  G  K  P  F  A  V  N  G  T  G

      190     200     210     220     230     240
   AGATGGCAACCCTTATGGTGAATACAGAGTTTGAAGCTTACCGTCGATGGCAACAAACC
      D  G  N  P  Y  G  G  I  Q  S  L  K  L  T  V  D  G  N  K  P

      250     260     270     280     290     300
   TCTGCCTTTTGCTTTTGATATCTTGTCAGCAGCATTCCAGTATGGCAACAGGGCATTAC
      L  P  F  A  F  D  I  L  S  A  A  F  Q  Y  G  N  R  A  F  T

      310     320     330     340     350     360
   CGAATACCCAAAAGAGATATCAGACTATTTCAAGCAGTCGTTTGAGTTTGGCGAGGGGTT
      E  Y  P  K  E  I  S  D  Y  F  K  Q  S  F  E  F  G  E  G  F

      370     380     390     400     410     420
   TACCTGGGAACGAAGTTTCACTTTTCAAGACGGGGCCATTTGCGTCGCCACGAACGATAT
      T  W  E  R  S  F  T  F  E  D  G  A  I  C  V  A  T  N  D  I

      430     440     450     460     470     480
   AAAGATGGTTGGCGATGAGTTTCAATATAACATTTCGATTGATGGTGTGAATTTCCCTGA
      K  M  V  G  D  E  F  Q  Y  N  I  R  F  D  G  V  N  F  P  E

      490     500     510     520     530     540
   AGATGGTCCWGTYATGCAGAAGAAAACGGTGAAGTGGGAGCCATCCACAGAGATAATGCC
      D  G  P  V  M  Q  K  K  T  V  K  W  E  P  S  T  E  I  M  R

      550     560     570     580     590     600
   TGTGCAAGGTGGAGTGCTAAAGGGTGAGGTTAACATGGCTCTGTTGCTTAAAGACAAAAG
      V  Q  G  G  V  L  K  G  E  V  N  M  A  L  L  L  K  D  K  S

      610     620     630     640     650     660
   CCATTACCGATGTGACTTCAAACTACTTACAAAGCTAAGAATCCTGTCCCGCCGACGGC
      H  Y  R  C  D  F  K  T  T  Y  K  A  K  N  P  V  P  P  T  A

      670     680     690     700     710     720
   GCTTCCAGACTACCACTATGTGGATCACTGTATTGAAATCACCGAGGAAAATAGGGATTA
      L  P  D  Y  H  Y  V  D  H  C  I  E  I  T  E  E  N  R  D  Y

      730     740     750     760     770     780
   CGTTAAGCTGCAGGAGTATGCTAAAGCTCGTTCTGGCCTGCACCTGCCCGAACTGCAAAA
      V  K  L  Q  E  Y  A  K  A  R  S  G  L  H  L  P  E  L  Q  K

      790     800     810
   GTAAAGGCTTAGGCGATAGTCAAGACGACAACGAGAAGA 3'
   *
```

(SEQ ID NO:09 & 10)

FIG. 13

Red fluorescent protein from *Ricordea florida* rfloRFP (AY037773)

```

      10      20      30      40      50      60
5' TGTGAAAGTTAACATTTTACTTTACTTCTACCAGCATGAGTGCACCTCAAAGAGGAAATGA
      M S A L K E E M K

      70      80      90     100     110     120
AAATCAAGCTTACATTGGTGGGCGTTGTTAACGGGCACCCATTCAAGATCATTGGGGACG
      I K L T L V G V V N G H P F K I I G D G

      130     140     150     160     170     180
GAAAAGGCAAACCTATGAGGGATCGCAGGAATTAACCTTGCCGTGGTGAAGGAGGGC
      K G K P Y E G S Q E L T L A V V E G G P

      190     200     210     220     230     240
CTCTGCCTTTCTCTTATGATATCCTGACAACGATAGTTCACCTATGGCAACAGGGCATTTG
      L P F S Y D I L T T I V H Y G N R A F V

      250     260     270     280     290     300
TGAAGTACCCAAAGGACATACCAGATATTTTCAAGCAGACCTGCTCTGGTCTGCTGCTG
      N Y P K D I P D I F K Q T C S G P G A G

      310     320     330     340     350     360
GATATTCCTGGCAAAGGACCATGAGTTTTGAAGACGGAGGCGTTTGCACTGCTACGAGCC
      Y S W Q R T M S F E D G G V C T A T S H

      370     380     390     400     410     420
ATATCAGGGTGGATGGCGACACTTTCAATTATGACATTCACCTTCATGGGAGCGGATTTCC
      I R V D G D T F N Y D I H F M G A D F P

      430     440     450     460     470     480
CTCTTAATGGTCCAGTGATGCAGAAAAGAACAGTGAAATGGGAGCCATCCACTGAGATAA
      L N G P V M Q K R T V K W E P S T E I M

      490     500     510     520     530     540
TGTTTTCAATGTGATGGATTGCTGAGGGGTGATGTTGCCATGTCTCTGTTGCTGAAAGGAG
      F Q C D G L L R G D V A M S L L L K G G

      550     560     570     580     590     600
GCGGCCATTACCGATGTGACTTTAAACTATTTATAAACCAAGAAGAATGTCAAGATGC
      G H Y R C D F K T I Y K P K K N V K M P

      610     620     630     640     650     660
CAGGTTACCATTTTGTGGACCACTGCATTGAGATAACGAGTCAACAGGACGATTACAACG
      G Y H F V D H C I E I T S Q Q D D Y N V

      670     680     690     700     710     720
TGGTTGAGCTGTACGAGGGTGCTGTAGCCCACTACTCTCTCTGCAGAAACCATGCCAAG
      V E L Y E G A V A H Y S P L Q K P C Q A

      730     740     750     760     770     780
CAAAGGCATAAAGCCAAACAACCCAAGAGGACAACAAGACATTTAATCAAATCACATCTT
      K A *

      790     800
TGTATTTTTTGGTTAGAGTTGAAAAAAA 3'

```

(SEQ ID NO:11 & 12)

FIG. 14

Green fluorescent protein from *Ricordea florida* rfloGFP (AY037772)

```

      10      20      30      40      50      60
5' AGTCACCTCGGTGTTTTTAGGACAGGAAGGATCACGAGCAAGAGAAGAAGTGTGAAAGTT
      70      80      90     100     110     120
AACACTTTACTCTACTTCTACCAGCATGAGTGCCTCAAAGAGGAAATGAAAATCAAGCT
                        M S A L K E E M K I K L

      130     140     150     160     170     180
TAAATGGTGGGCGTTGTTAACGGGCAGTCATTTTCAGATCGATGGGGAAGGAAAAGGCAA
K M V G V V N G Q S F Q I D G E G K G K

      190     200     210     220     230     240
ACCTTACGAGGGATCACAGAAATTAACCTTGAAGTGGTGAAGGAGGCCTCTGCTCTT
P Y E G S Q K L T L E V V E G G P L L F

      250     260     270     280     290     300
CTCTTATGATATCCTGACAACGATATTTTCAGTATGGCAACAGGGCATTCGTGAAGTACCC
S Y D I L T T I F Q Y G N R A F V N Y P

      310     320     330     340     350     360
AAAGGACATACCAGATATTTTCAAGCAGACCTGCTCTGGTCCTGATGGTGGATTTTCCTG
K D I P D I F K Q T C S G P D G G F S W

      370     380     390     400     410     420
GCAAAGGACCATGACTTATGAAGACGGAGGGGTTTGCCTGCTTCAAACCATCAGCGT
Q R T M T Y E D G G V C T A S N H I S V

      430     440     450     460     470     480
GGACGGCGACACTTTTTTATTATGTGATAAGATTTAATGGAGAGAATTTTCCTCCAAATGG
D G D T F Y Y V I R F N G E N F P P N G

      490     500     510     520     530     540
TCCAGTAATGCAGAAAAGAACAGTGAAATGGGAGCCATCCACTGAGATAATGTTTGAACG
P V M Q K R T V K W E P S T E I M F E R

      550     560     570     580     590     600
TGATGGATTGCTGAGGGGTGACATTGCCATGTCTCTGTTGCTGAAAGGAGGCGGCCATTA
D G L L R G D I A M S L L L K G G H Y

      610     620     630     640     650     660
CCGATGTGACTTTTAAACTATTTTATACACCCAAGAGGAAGGTCAACATGCCAGGTTACCA
R C D F K T I Y T P K R K V N M P G Y H

      670     680     690     700     710     720
TTTTGTGGACCACTGCATTGAGATACAGAAGCACGACAAGGATTACAACATGGCTGTGCT
F V D H C I E I Q K H D K D Y N M A V L

      730     740     750     760     770     780
CTCTGAGGATGCTGTAGCCCACTCTCTCTGGAGAAAAAAGCCAAGCAAAGGCGTA
S E D A V A H N S P L E K K S Q A K A *

      790
AAGCCAAACAACCTAA 3'

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(SEQ ID NO:13&14)

FIG. 15

Red fluorescent protein from *Montastraea cavernosa* mcavRFP (AY037770)

```

      10      20      30      40      50      60
5'ACGCAGGGATTACCCCTGGTGATTTGGAAGAGAGCAGACCGAGAACAACAAGAGCTGTAT
      70      80      90     100     110     120
AAGGCTGATATCTTACTTTACGTCTACCATCATGAGTGTGATTAAATCAGTCATGAAGAT
R  L  I  S  Y  F  T  S  T  I  M  S  V  I  K  S  V  M  K  I

      130     140     150     160     170     180
CAAGCTGCGTATGGAAGGCAGTGTAACCGGCACAACCTTCGTAATTGTTGGAGAAGGAGA
K  L  R  M  E  G  S  V  N  G  H  N  F  V  I  V  G  E  G  E

      190     200     210     220     230     240
AGGCAAGCCTTATGAGGGAACACAGAGTATGGACCTTACAGTCAAAGAAGGCGCACCTCT
G  K  P  Y  E  G  T  Q  S  M  D  L  T  V  K  E  G  A  P  L

      250     260     270     280     290     300
GCCTTTCGCCTACGATATCATGACAACAGTATTCCATTACGGCAATAGGGTATTCGCAAA
P  F  A  Y  D  I  M  T  T  V  F  H  Y  G  N  R  V  F  A  K

      310     320     330     340     350     360
ATACCCAAAACATATCCCAGACTATTTCAAGCAGATGTTTCCTGAGGAGTATTCCTGGGA
Y  P  K  H  I  P  D  Y  F  K  Q  M  F  P  E  E  Y  S  W  E

      370     380     390     400     410     420
ACGAAGCATGAATTTCTGAAGGCGGGGGCATTTGCACCGCCAGGAACGAGATAACAATGGA
R  S  M  N  F  E  G  G  G  I  C  T  A  R  N  E  I  T  M  E

      430     440     450     460     470     480
AGGCGACTGTTTTTCAATAAAGTTTCGATTTGATGGTGTGAACTTCCCCCAATGGTCC
G  D  C  F  F  N  K  V  R  F  D  G  V  N  F  P  P  N  G  P

      490     500     510     520     530     540
AGTCATGCAGAAGAAGACGCTGAAATGGGAGCCATCCACTGAAAAAATGTATGTGCGTGA
V  M  Q  K  K  T  L  K  W  E  P  S  T  E  K  M  Y  V  R  D

      550     560     570     580     590     600
TGGAGTGCTGACGGGTGATATCAACATGGCTTTGTTGCTTGAAGGAGGTGGCCATTACCG
G  V  L  T  G  D  I  N  M  A  L  L  L  E  G  G  G  H  Y  R

      610     620     630     640     650     660
ATGTGACTTCAGAACTACTTACAGAGCTAAGAAGAAGGGTGTCAAGTTACCAGATTATCA
C  D  F  R  T  T  Y  R  A  K  K  K  G  V  K  L  P  D  Y  H

      670     680     690     700     710     720
CTTTGAGGATCACTCCATTGAGATTTTTCGCCATGACAAAGAATACACTGAGGTTAAGCT
F  E  D  H  S  I  E  I  L  R  H  D  K  E  Y  T  E  V  K  L

      730     740     750     760     770     780
GTATGAGCATGCCGAAGCTCATTTCTGGGCTGCCGAGGGTGGCAAAGTAAAGGCTTAACGA
Y  E  H  A  E  A  H  S  G  L  P  R  V  A  K  *

      790
AAAGCCAAGACCACA 3'

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(SEQ ID NO:15 & 16)

FIG. 16

Green fluorescent protein from *Montastraea cavernosa* mcavGFP (AY037769)

```

      10      20      30      40      50      60
5' ATTCGCCCTGGTGATTGGAAGAGAGCAGATCGAGAACAACAAGAGCTGTAAGGTTGATA
      70      80      90     100     110     120
   TCTTACTTACGTCTACCATCATGACAAGTGTGTCACAGGAAAAGGGTGTGATTAAACCAG
               M  T  S  V  A  Q  E  K  G  V  I  K  P  D

      130     140     150     160     170     180
   ACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGGCACAAGTTCGTGGTTGAAG
       M  K  M  K  L  R  M  E  G  A  V  N  G  H  K  F  V  V  E  G

      190     200     210     220     230     240
   GAGATGGAAAAGGGAAGCCTTTCGACGGAACACAGACTATGGACCTTACAGTCATAGAAG
       D  G  K  G  K  P  F  D  G  T  Q  T  M  D  L  T  V  I  E  G

      250     260     270     280     290     300
   GCGCACCATTGCCTTTCGCTTACGATATCTTGACAACAGTATTCGATTACGGCAACAGGG
       A  P  L  P  F  A  Y  D  I  L  T  T  V  F  D  Y  G  N  R  V

      310     320     330     340     350     360
   TATTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAGCAGACGTTTCCTGAGGGGT
       F  A  K  Y  P  E  D  I  A  D  Y  F  K  Q  T  F  P  E  G  Y

      370     380     390     400     410     420
   ACTTCTGGAACGAAGCATGACATACGAAGACCAGGGCATTTCGATCGCCACAAACGACA
       F  W  E  R  S  M  T  Y  E  D  Q  G  I  C  I  A  T  N  D  I

      430     440     450     460     470     480
   TAACAATGATGGAAGGCGTCGACGACTGTTTTGCCTATAAAATTTCGATTTGATGGTGTGA
       T  M  M  E  G  V  D  D  C  F  A  Y  K  I  R  F  D  G  V  N

      490     500     510     520     530     540
   ACTTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTGAAATGGGAGCCATCCACTG
       F  P  A  N  G  P  V  M  Q  R  K  T  L  K  W  E  P  S  T  E

      550     560     570     580     590     600
   AGATAATGTATGCGCGTGATGGAGTGCTGAAGGGTGATGTTAACATGGCTCTGTTGCTTG
       I  M  Y  A  R  D  G  V  L  K  G  D  V  N  M  A  L  L  L  E

      610     620     630     640     650     660
   AAGGAGGTGGCCATTACCGATGTGACTTCAAACTACTTACAAAGCTAAGAAGGTTGTCC
       G  G  G  H  Y  R  C  D  F  K  T  T  Y  K  A  K  K  V  V  R

      670     680     690     700     710     720
   GGTTGCCAGACTATCACTTTGTGGACCATGCGATTGAGATTGTGAGCCACGACAAAGATT
       L  P  D  Y  H  F  V  D  H  R  I  E  I  V  S  H  D  K  D  Y

      730     740     750     760     770     780
   ACAACAAGGTTAAGCTGCACGAGCATGCCGAAGCTCGTCATGGACTGTCAAGGAAGGCCA
       N  K  V  K  L  H  E  H  A  E  A  R  H  G  L  S  R  K  A  K

      790     800     810     820     830     840
   AGTAAAGGCTTAATGAAAAGTCAAGACGACAACGAGGAGAAACAAAGTACTTTTTTGTTA
       *

      850     860     870     880     890     900
   AATTTGAAGGCATTTACTCGGAATTAGTATTTGATACTTTCGATTCAAGGATTGTTCGG
       910     920     930     940     950     960
   GGATTTGTTAGAGACTAGCTCTAGAGTTGTATTTTGTGAAAAAGATAGTTTCCAGTTT
       970     980     990    1000    1010    1020
   TGCGGGATTACAGCATGGGGATAGACTTTTTTAAACTCAGTTGTGGTCAAATGCAAGTAAG
       1030    1040    1050    1060
   AAACTGTAGTGAGAATAAACTTGTATCGAAGCCGAAAAAAAAA 3'
   (SEQ ID NOS: 17 & 18)

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FIG. 17

Green fluorescent protein from *Condylactis gigantea* cgigGFP (AY037776)

```

5' ACAGCTGTT 10 20 30 40 50 60
    CATCCACGCTCATTCAAGACGCCGTCAACTTTATTCCAGTCAGGAAAATGT
                                     M Y

    70 80 90 100 110 120
    ATCCTTGGATCAAGGAAACCATGCGCAGTAAGGTTTACATGGAAGGAGATGTTAACAACC
    P W I K E T M R S K V Y M E G D V N N H

    130 140 150 160 170 180
    ACGCCTTCAAGTGCAGTGCAGTAGGAGAAGGAAAACCATACAAAGGCTCACAAGACCTGA
    A F K C T A V G E G K P Y K G S Q D L T

    190 200 210 220 230 240
    CGATTACCGTCACTGAAGGAGGTCTCTGCCATTTGCTTTTCGACATTCTTTCACACGCCT
    I T V T E G G P L P F A F D I L S H A F

    250 260 270 280 290 300
    TTCAGTATGGCAACAAGGTGTTCAACCGATTACCCCGACGATATTCCTGATTTCTTTAAGC
    Q Y G N K V F T D Y P D D I P D F F K Q

    310 320 330 340 350 360
    AGTCTCTCTCGGATGGTTTACTTGGAGAAGAGTAAGCACSTATGACGATGGAGGAGTCC
    S L S D G F T W R R V S T Y D D G G V L

    370 380 390 400 410 420
    TCACAGTTACCCAAGACACTAGTCTGAAGGGAGATTGCATTATTTGCAACATTAAAGTCC
    T V T Q D T S L K G D C I I C N I K V H

    430 440 450 460 470 480
    ATGGCACTAACTTCCCCGAAAATGGTCCGGTGATGCAAAACAAGACCGATGGATGGGAGC
    G T N F P E N G P V M Q N K T D G W E P

    490 500 510 520 530 540
    CATCCAGCACTGAAACGGTTATTCCACAAGATGGAGGAATTGTTGCTGCGCGATCACCCG
    S S T E T V I P Q D G G I V A A R S P A

    550 560 570 580 590 600
    CACTAAGGCTGCGTGATAAAGGTCACTTATCTGCCACATGGAAACAACCTACAAGCCAA
    L R L R D K G H L I C H M E T T Y K P N

    610 620 630 640 650 660
    ACAAAGAGGTGAAGCTGCCAGAACTCCACTTTCATCATTTGCGAATGGAAAAGCTGAGTG
    K E V K L P E L H F H H L R M E K L S V

    670 680 690 700 710 720
    TTAGTGACGATGGGAAGACCATTAAAGCAGCAGAGTATGTGGTGGCTAGCTACTCCAAAG
    S D D G K T I K Q H E Y V V A S Y S K V

    730 740 750 760 770 780
    TGCCTTCGAAGATAGGACGTCAATGATCATTTCCCTTATTAAATATCAATGATGTGGCTT
    P S K I G R Q *

    790 800 810 820 830 840
    TCAATTTTCCAAAATTTTGTAAAGACATAGGTCTTTTGGATTTTGGTAACCCCAACCTT
    850 860 870 880 890
    AATCCCAATAATTTTGTGGAAAGTCAAATAAAACCAGCCTTCCCTGGGCCTTTAA 3'
  
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(SEQ ID NOS: 19 & 20)

FIG. 18

Green fluorescent protein from *Agaricia fragilis* afraGFP (AY037765)

```

      10      20      30      40      50      60
5' CAAGGAAGCCAAATCTTTTACCAGAGATCTCGCGTGAAAGCAACCTATGAGTGATGGCGA
                                     M A I

      70      80      90     100     110     120
TTTCTACTCTAAAGAACGTCATCATCATCGTTATTATATACTCCTGCAGCACTTGTGCTG
  S T L K N V I I I V I I Y S C S T C A V

     130     140     150     160     170     180
TTTGGTTCGAATTCAAACTCTGAATCCTCTTTCACTAATGGGATTGCAGAGGAAATGAAGA
  W S N S N S E S S F T N G I A E E M K T

     190     200     210     220     230     240
CTAGGGTACATTTGGAGGGTACTGTTAACGGGCACTCCTTTACAATTAAAGGCGAAGGAA
  R V H L E G T V N G H S F T I K G E G R

     250     260     270     280     290     300
GAGGCTACCCCTTACAAAGGAGAACAGTTTATGAGCCTTGAGGTCGTCAATGGTGCTCCTC
  G Y P Y K G E Q F M S L E V V N G A P L

     310     320     330     340     350     360
TGCCGTTCTCTTTTGATATCTTGACACCAGCATTTATGTATGGCAACAGAGTGTTCACCA
  P F S F D I L T P A F M Y G N R V F T K

     370     380     390     400     410     420
AGTACCCACCAAACATACCAGACTATTTCAAGCAGACGTTTCCTGAAGGGTATCACTGGG
  Y P P N I P D Y F K Q T F P E G Y H W E

     430     440     450     460     470     480
AAAGAAACATTCCCTTTGAAGATCAGGCCGCGTGCACGGTAACCAGCCACATAAGATTGG
  R N I P F E D Q A A C T V T S H I R L E

     490     500     510     520     530     540
AAGAGGAAGAGAGGCGTTTTGTAAATAACGTCAGATTTCACTGTGTGAACCTTTCCCCCTA
  E E E R R F V N N V R F H C V N F P P N

     550     560     570     580     590     600
ATGGTCCAGTCATGCAGAGGAGGATACTGAAATGGGAGCCATCCACTGAGAACATTTATC
  G P V M Q R R I L K W E P S T E N I Y P

     610     620     630     640     650     660
CGCGTGATGGGTTTTCTGGAGGGCCATGTTGATATGACTCTTCGGGTTGAAGGAGGTGGCT
  R D G F L E G H V D M T L R V E G G G Y

     670     680     690     700     710     720
ATTACCGAGCTGAGTTCAAAAGTACTTACAAAGGGAAGACCCAGTCCGCGACATGCCAG
  Y R A E F K S T Y K G K T P V R D M P D

     730     740     750     760     770     780
ACTTTCACTTCATAGACCACCGCATTGAGATTACGGAGCATGACGAAGACTACACCAATG
  F H F I D H R I E I T E H D E D Y T N V

     790     800     810     820     830     840
TTGAGCTGCATGACGTATCCTGGGCTCGTTACTCTATGCTGCCGACTATGTAAGCGGAAA
  E L H D V S W A R Y S M L P T M

     850     860     870     880     890     900
AGGCAAGGCAACAAGACGCAAAACCGCCCTGTTTGTCTCTTTTCATAAGAGATTTGACAA
  910     920     930     940     950     960
CCGTGGTTCCTTTGCCATTTAATTGAATTAGTTTAAATTAATCTTTGGGATTGATGTAG
  970     980     990     1000    1010    1020
ACGCTTTGGTTGCTAAGTAAGAAAACATTTGTGATTATTAAATTTGTTGCCTGAAGCAAA
  1030
AAAAAAAAA 3'

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(SEQ ID NOS:21 & 22)

FIG. 19

Green fluorescent protein from *Ricordea florida* rfloGFP2 (AY037774)

```

      10      20      30      40      50      60
5' AGCCACTTCGGTGTCTTGTCTCGAGAGGAAGGATCACGAACAAGAGAAGAGCTGTAAAAGTT
      70      80      90     100     110     120
   AAAATTTTACTTTACTTCTTCCAGCATGAATGCACTTCAAGAGGAAATGAAAATCAAGCT
                        M  N  A  L  Q  E  E  M  K  I  K  L

      130     140     150     160     170     180
   TACAATGGTGGGCGTTGTAAACGGGCAGTCATTTAAGATCGATGGGAAAAGGAAAAGGGAA
   T  M  V  G  V  V  N  G  Q  S  F  K  I  D  G  K  G  K  G  K

      190     200     210     220     230     240
   ACCTTACGAGGGATCACAGGAATTGACCCTTAAAGTGGTGGAAGGCGGGCCTCTGCTCTT
   P  Y  E  G  S  Q  E  L  T  L  K  V  V  E  G  G  P  L  L  F

      250     260     270     280     290     300
   CTCTTATGATATCCTGACAACGATATTTTCAGTATGGCAACAGGGCATTTCGTGAAC TACCC
   S  Y  D  I  L  T  T  I  F  Q  Y  G  N  R  A  F  V  N  Y  P

      310     320     330     340     350     360
   AAAGGACATACCAGATATTTTCAAGCAAACGTGTTCTGGTCTTGATGGCGGATATTCGTG
   K  D  I  P  D  I  F  K  Q  T  C  S  G  L  D  G  G  Y  S  W

      370     380     390     400     410     420
   GCAAAGGACCATGACTTATGAGGACGGAGGGGTTTGTACTGCTACAAGCAACGTCAGCGT
   Q  R  T  M  T  Y  E  D  G  G  V  C  T  A  T  S  N  V  S  V

      430     440     450     460     470     480
   GGTCGGCGACACTTTTCAATTATGAAATTCAC TTTATGGGGGCGAATTTTCCTCCAAATGG
   V  G  D  T  F  N  Y  E  I  H  F  M  G  A  N  F  P  P  N  G

      490     500     510     520     530     540
   TCCRGTGATGCAGAAAAGAACAGTGAAGTGGGAGCCCTCCACTGAGATAATGTTTGAACG
   P  V  M  Q  K  R  T  V  K  W  E  P  S  T  E  I  M  F  E  R

      550     560     570     580     590     600
   TGATGGATTGCTGAGGGGTGATGTTCCCATGTCTCTGTTGCTGAAAGGAGGCGACCATTA
   D  G  L  L  R  G  D  V  P  M  S  L  L  L  K  G  G  D  H  Y

      610     620     630     640     650     660
   CCGATGTGACTTTTAAACTATTTATAAACCCAACAAGAAGGTCAAGCTGCCAGGTTACCA
   R  C  D  F  K  T  I  Y  K  P  N  K  K  V  K  L  P  G  Y  H

      670     680     690     700     710     720
   TTTTGTGGACCACTGCATTGAGATAAAGAGTCAAGAGAATGATTACAACATGGTTGCGCT
   F  V  D  H  C  I  E  I  K  S  Q  E  N  D  Y  N  M  V  A  L

      730     740     750     760     770     780
   CTTTGAGGATGCTGTAGCACACTACTCTCCTCTGGAGAAAAAGAGCCAGGCAAAGGCGTA
   F  E  D  A  V  A  H  Y  S  P  L  E  K  K  S  Q  A  K  A  *

      790     800     810     820     830     840
   AATCCAAACAACCTAAGAAGACGACAAGGCATTCAATCTAATCGCATGTTTGAATTTTGTG
   850     860     870     880     890     900
   GTTAGGAATGTGTTGGGTCTAGGTCTAGAACGTTTTCATTTTGGCTGGATTTGTTT
   910     920     930     940     950     960
   ACTCAGTTATAGACAAGAAAAAATCTTAAATGACTTGGGTTGGATTAGCTTTTCGGGCAC
   970     980     990     1000    1010    1020
   TGTCAATTCCGGATTCCCTTAGAAATATTTGAGACCAAGCCTTTTTTTTGAGCTGAGAACGT
   AATC 3'

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(SEQ ID NOS: 23 & 24)

FIG. 20

Green fluorescent protein from *Montastraea cavernosa* mcavGFP2 (AY037768)

```

      10      20      30      40      50      60
5' AGAGCTGTAGGGTGATATCTTACTTACGTCTACCATCATGACCAGTGTTCACAGGAAAA
      M T S V A Q E K

      70      80      90     100     110     120
GGGTGTGATTAAACCAGACATGAAGATGAAGCTGCGTATGGAAGGTGCTGTAAACGGGCA
G V I K P D M K M K L R M E G A V N G H

      130     140     150     160     170     180
CAAGTTCGTGATTGAAGGAGATGGAAAAGGGAAGCCTTTCGACGGAACACAGACTATGGA
K F V I E G D G K G K P F D G T Q T M D

      190     200     210     220     230     240
CCTTACAGTCATAGAAGGCGCACCATTGCCTTTTCGCTTACGCTATCTTGACAACAGTATT
L T V I E G A P L P F A Y A I L T T V F

      250     260     270     280     290     300
CGATTACGGCAACAGGGTATTCGCCAAATACCCAGAAGACATAGCAGATTATTTCAAGCA
D Y G N R V F A K Y P E D I A D Y F K Q

      310     320     330     340     350     360
GACATTTCTCTGAGGGGTACTTCTGGGAACGAAGCATGACATACGAAGACCAGGGCATTTC
T F P E G Y F W E R S M T Y E D Q G I C

      370     380     390     400     410     420
CATCGCCACAAACGACATAACAATGATGAAAGGCGTCGACGACTGTTTTGTCTATAAAAT
I A T N D I T M M K G V D D C F V Y K I

      430     440     450     460     470     480
TCGATTTCGATGGTGTGAACCTTTCCTGCCAATGGTCCAGTTATGCAGAGGAAGACGCTGAA
R F D G V N F P A N G P V M Q R K T L K

      490     500     510     520     530     540
ATGGGAGCCATCCACTGAGAAAATGTATGCGCGTGATGGAGTGCTGAAGGGTGATGTTAA
W E P S T E K M Y A R D G V L K G D V N

      550     560     570     580     590     600
CATGGCTCTGTTGCTTGAAGGAGGTGGCCATTACCGATGTGACTTCAAACTACTTACAG
M A L L L E G G G H Y R C D F K T T Y R

      610     620     630     640     650     660
AGCTAAGAAGGTTGTCCAGTTGCCAGACTATCATTTTGTGGACCATCGCATTGAGATTGT
A K K V V Q L P D Y H F V D H R I E I V

      670     680     690     700     710     720
GAGCCACGACAAAGATTACAACAAGGTTAAGCTGTATGAGCATGCCGAAGCTCATTCTGG
S H D K D Y N K V K L Y E H A E A H S G

      730     740     750     760     770     780
GCTGCCGAGGCAGGCCAAGTAAAGGCTTAATGAAAAGCCAAGACGACAACAAGGAGAAAC
L P R Q A K *

      790     800     810     820     830     840
AAAGTATTTTTTTTGTAAATTTCAAGGCATTTACTCGGAATTAGTATTTGATACTTTTCG
      850     860     870     880     890     900
ATTCAAGGATTTGTTTCGGGACTTGTTAGAGACCAGCTCTAGAGTTGTATTTTGTGAAAA
      910
AAAGATAGTTTCC 3'

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(SEQ ID NOS: 25 & 26)

FIG. 21

Green fluorescent protein homolog from *Montastraea annularis* mannFP (AY037766)

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      10      20      30      40      50      60
5' TGGTTAACGCAGAGTCGCGGGGGTTCCTGGCTAATAATTGATTCTATTTTGGGTGTGAC
      70      80      90     100     110     120
   ATTCAGGTTTAAAGCAGCATCCTCAGTGCTGAGGTCTCATTACCCTGGTGATTTGGAAG
      130     140     150     160     170     180
   AGAGCAGATCGAGAACACCAAGAGCTGTATTACGCTAAAAATCTTACTTGCCCTCTACCACC
      190     200     210     220     230     240
   ATGAGTATGATTAAACCAGAAATGAAGATCAAGATGCGTATGGACGGTGCTGTAAACGGG
M  S  M  I  K  P  E  M  K  I  K  M  R  M  D  G  A  V  N  G

      250     260     270     280     290     300
   CACAAGTTCGTGATTACAGGGGAAGGAAGCGGCGAGCCTTTCGAGGGAAACAGACTATG
H  K  F  V  I  T  G  E  G  S  G  E  P  F  E  G  K  Q  T  M

      310     320     330     340     350     360
   AACCTGACAGTCATAGACGGCGGACCTCTGCCTTTCGCTTTCGACATCTTGACAACAGCA
N  L  T  V  I  D  G  G  P  L  P  F  A  F  D  I  L  T  T  A

      370     380     390     400     410     420
   TTCGATTACGGCAGGAGGTATTCGCCAAATACCCAGAAGACATCCAGACTATTTCAAG
F  D  Y  G  X  R  V  F  A  K  Y  P  E  D  I  P  D  Y  F  K

      430     440     450     460     470     480
   CAGTCGTTTCCTGAGGGGTTTTCTTGGAACGAAGCATGACTTACGAAGACGGGGGCATT
Q  S  F  P  E  G  F  S  W  E  R  S  M  T  Y  E  D  G  G  I

      490     500     510     520     530     540
   TGCATCGCCACAAATGACATAAAAAATGGAAGGCGACTGCTTTTCCTATGAAATTGATTT
C  I  A  T  N  D  I  K  M  E  G  D  C  F  S  Y  E  I  R  F

      550     560     570     580     590     600
   GATGGGGTGAACTTTCCTGCCAATAGTCCAGTTATGCAGAAGAAGACCGTGAAATGGGAG
D  G  V  N  F  P  A  N  S  P  V  M  Q  K  K  T  V  K  W  E

      610     620     630     640     650     660
   CCATGCACTGRGAAATGTATGTGCGTGATGGAGTGCTTAAAGGTGGTCTTAACATGGCT
P  C  T  X  E  M  Y  V  R  D  G  V  L  K  G  G  L  N  M  A

      670     680     690     700     710     720
   CTGTTGCTTGAAGGAGGTGGCCATTTCCGATGTGACTTGAAAACCTACTTACAAAGCTAAG
L  L  L  E  G  G  G  H  F  R  C  D  L  K  T  T  Y  K  A  K

      730     740     750     760     770     780
   AAGGTTGTCCAGATGCCAGACTATCACTTTGTGAATCACCGACTTGAGATAACATGGCAT
K  V  V  Q  M  P  D  Y  H  F  V  N  H  R  L  E  I  T  W  H

      790     800     810     820     830     840
   GACGAGGATTACAACAATGTTAAGCTGTCTGAGCATGCAGAAGCTCATTCTGGACTGCCA
D  E  D  Y  N  N  V  K  L  S  E  H  A  E  A  H  S  G  L  P

      850     860     870     880     890     900
   AGGCAGGCCAAATAAAGGCTTGACGAAAAGCCAAAACGGCAAAGAGTACAAGAAAGTATA
R  Q  A  K  *

      910     920     930     940     950     960
   TATAAATGTATATTTTTCAACTGAAAGGCATTCCACTCGGAATTAGTATTTGATACTTTC
      970     980     990     1000    1010    1020
   AATTCAAGGATTTATTTTGGGATTTGCTAGCCACTAGCTTTATTGTTAAATTAAGTTAAA
      1030    1040    1050    1060    1070    1080
   GACGGTTTAGCATTTTTTCGGTATTACAACATAGGCACAGACGTCTTAACCCAGTAGTG
      1090    1100    1110    1120    1130
   GTCAGGTACAAGTAAGAAAACCTTTGGTGAGAATAGACTTGTAGTCGAAAAAAA 3'

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(SEQ ID NOS:27 & 28)